

SEQUENCE LISTING

<110> Markham and Bonthron

<120> Wound Healing and Orofacial Clefting

<130> 59367

<140> 09/869,564

<141> 2001-06-29

<150> PCT/GB00/000003

<151> 2000-01-06

<150> GB9900167.9

<151> 1999-01-06

<160> 39

<170> PatentIn Ver. 2.1

<210> 1

<211> 4997

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (85) .. (2283)

<400> 1

ggaggattcg cagttcaaca tcaagggtccc tgtgcgtttt attgcgacct gccggtggga 60

actttgtctc cgagtcggag cagc atg gag cgg cgg agc gag agc ccg tgt 111
 Met Glu Arg Arg Ser Glu Ser Pro Cys
 1 5

ctg cgg gac agc ccc gac cgg cgg agc ggc agc ccg gac gtc aag ggg 159
 Leu Arg Asp Ser Pro Asp Arg Arg Ser Gly Ser Pro Asp Val Lys Gly
 10 15 20 25

cct ccc cca gtg aag gtg gcc cgg ctg gag cag aac ggc agc ccc atg 207
 Pro Pro Pro Val Lys Val Ala Arg Leu Glu Gln Asn Gly Ser Pro Met
 30 35 40

gga gcc cgc ggg agg ccc aac ggc gcc gtg gcc aag gcc gtg gga ggt 255
 Gly Ala Arg Gly Arg Pro Asn Gly Ala Val Ala Lys Ala Val Gly Gly
 45 50 55

ttg atg att cct gtc ttt tgt gtc gtg gag cag ttg gac ggc tct ctt 303
 Leu Met Ile Pro Val Phe Cys Val Val Glu Gln Leu Asp Gly Ser Leu
 60 65 70

gaa tat gac aac aga gaa gaa cac gcc gag ttt gtc ctg gtg cgg aaa 351
 Glu Tyr Asp Asn Arg Glu Glu His Ala Glu Phe Val Leu Val Arg Lys
 75 80 85

```

gat gtg ctt ttt agc cag ctg gtg gag act gcg ctc ctg gcc ctg ggg 399
Asp Val Leu Phe Ser Gln Leu Val Glu Thr Ala Leu Leu Ala Leu Gly
90 95 100 105

tat tct cac agc tct gcg gcc cag gcc caa gga ata atc aag ctg gga 447
Tyr Ser His Ser Ser Ala Ala Gln Ala Gln Gly Ile Ile Lys Leu Gly
110 115 120

agg tgg aac cct ctc ccc ctc agt tat gtg aca gat gca ccc gac gcg 495
Arg Trp Asn Pro Leu Pro Leu Ser Tyr Val Thr Asp Ala Pro Asp Ala
125 130 135

aca gtg gcc gac atg cta caa gat gtc tat cat gtt gtg acg ttg aaa 543
Thr Val Ala Asp Met Leu Gln Asp Val Tyr His Val Val Thr Leu Lys
140 145 150

atc caa tta caa agt tgt tca aag ttg gaa gac ttg cct gcg gag cag 591
Ile Gln Leu Gln Ser Cys Ser Lys Leu Glu Asp Leu Pro Ala Glu Gln
155 160 165

tgg aac cat gcc aca gtc cgc aat gcc tta aag gaa ctg ctc aaa gag 639
Trp Asn His Ala Thr Val Arg Asn Ala Leu Lys Glu Leu Leu Lys Glu
170 175 180 185

atg aac cag agc aca tta gcc aaa gaa tgc cct ctc tcc cag agt atg 687
Met Asn Gln Ser Thr Leu Ala Lys Glu Cys Pro Leu Ser Gln Ser Met
190 195 200

att tca tcc att gta aat agc aca tat tat gcc aat gtg tca gca acc 735
Ile Ser Ser Ile Val Asn Ser Thr Tyr Tyr Ala Asn Val Ser Ala Thr
205 210 215

aag tgc cag gag ttt ggg aga tgg tat aaa aag tac aag aag att aaa 783
Lys Cys Gln Glu Phe Gly Arg Trp Tyr Lys Lys Tyr Lys Lys Ile Lys
220 225 230

gtg gaa aga gtg gaa cga gaa aac ctt tca gac tat tgt gtt ctg ggc 831
Val Glu Arg Val Glu Arg Glu Asn Leu Ser Asp Tyr Cys Val Leu Gly
235 240 245

cag cgt cca atg cat tta cca aat atg aac cag ctg gca tcc ctg ggg 879
Gln Arg Pro Met His Leu Pro Asn Met Asn Gln Leu Ala Ser Leu Gly
250 255 260 265

aaa acc aac gaa cag tct cct cac agc caa att cac cac agt act cca 927
Lys Thr Asn Glu Gln Ser Pro His Ser Gln Ile His His Ser Thr Pro
270 275 280

atc cga aac caa gtg ccc gca tta cag ccc atc atg agc cct ggt ctt 975
Ile Arg Asn Gln Val Pro Ala Leu Gln Pro Ile Met Ser Pro Gly Leu
285 290 295

ctt tct ccc cag ctt agt cca caa ctt gta agg caa caa ata gcc atg 1023
Leu Ser Pro Gln Leu Ser Pro Gln Leu Val Arg Gln Gln Ile Ala Met
300 305 310

gcc cat ctg ata aac caa cag att gcc gtt agc cgg ctc ctg gct cac 1071

```

Ala His Leu Ile Asn Gln Gln Ile Ala Val Ser Arg Leu Leu Ala His
 315 320 325

cag cat cct caa gcc atc aac cag cag ttc ctg aac cat cca ccc atc 1119
 Gln His Pro Gln Ala Ile Asn Gln Gln Phe Leu Asn His Pro Pro Ile
 330 335 340 345

ccc aga gca gtt aag cca gag cca acc aac tct tcc gtg gaa gtc tct 1167
 Pro Arg Ala Val Lys Pro Glu Pro Thr Asn Ser Ser Val Glu Val Ser
 350 355 360

cca gat atc tac cag caa gtc aga gat gag ctg aag agg gcc agt gtg 1215
 Pro Asp Ile Tyr Gln Gln Val Arg Asp Glu Leu Lys Arg Ala Ser Val
 365 370 375

tcc caa gct gtc ttt gca aga gtg gca ttc aac cgc aca cag gga ttg 1263
 Ser Gln Ala Val Phe Ala Arg Val Ala Phe Asn Arg Thr Gln Gly Leu
 380 385 390

ttg tot gag att ctg cgt aag gaa gaa gac cct cgg aca gcc tct cag 1311
 Leu Ser Glu Ile Leu Arg Lys Glu Glu Asp Pro Arg Thr Ala Ser Gln
 395 400 405

tct ctt cta gta aac ctg agg gcc atg cag aat ttc ctc aat ctg cca 1359
 Ser Leu Leu Val Asn Leu Arg Ala Met Gln Asn Phe Leu Asn Leu Pro
 410 415 420 425

gaa gtg gag cga gat cgc atc tac cag gat gag agg gag cgg agc atg 1407
 Glu Val Glu Arg Asp Arg Ile Tyr Gln Asp Glu Arg Glu Arg Ser Met
 430 435 440

aat ccc aat gtg agc atg gtc tcc tcg gcc tcc agc agt ccc agc tcc 1455
 Asn Pro Asn Val Ser Met Val Ser Ser Ala Ser Ser Ser Pro Ser Ser
 445 450 455

tcc cga acc cct cag gcc aaa acc tcg aca ccg aca aca gac ctc cct 1503
 Ser Arg Thr Pro Gln Ala Lys Thr Ser Thr Pro Thr Thr Asp Leu Pro
 460 465 470

att aag gtg gac ggc gcc aac atc aac atc aca got gcc att tat gac 1551
 Ile Lys Val Asp Gly Ala Asn Ile Asn Ile Thr Ala Ala Ile Tyr Asp
 475 480 485

gag atc caa cag gag atg aaa agg gcc aag gtg tct caa gcc ctg ttt 1599
 Glu Ile Gln Gln Glu Met Lys Arg Ala Lys Val Ser Gln Ala Leu Phe
 490 495 500 505

gcc aaa gtg gct gca aat aaa agt cag ggc tgg ctg tgt gaa ctg ctc 1647
 Ala Lys Val Ala Ala Asn Lys Ser Gln Gly Trp Leu Cys Glu Leu Leu
 510 515 520

cgc tgg aag gag aac cca agc cca gaa aac cgc acc ctc tgg gaa aac 1695
 Arg Trp Lys Glu Asn Pro Ser Pro Glu Asn Arg Thr Leu Trp Glu Asn
 525 530 535

ctc tgt acc atc cgt cgc ttc ctg aac ctt ccc cag cat gag agg gat 1743
 Leu Cys Thr Ile Arg Arg Phe Leu Asn Leu Pro Gln His Glu Arg Asp

| 540 | 545 | 550 | |
|--------------------------------------------------------------------|-----|-----|------|
| gtc atc tat gag gag gag tca agg cat cac cac agc gaa cgc atg caa | | | 1791 |
| Val Ile Tyr Glu Glu Glu Ser Arg His His His Ser Glu Arg Met Gln | | | |
| 555 | 560 | 565 | |
| cac gtg gtc cag ctt ccc cct gag ccg gtg cag gta ctt cat aga cag | | | 1839 |
| His Val Val Gln Leu Pro Pro Glu Pro Val Gln Val Leu His Arg Gln | | | |
| 570 | 575 | 580 | 585 |
| cag tct cag cca gcc aag gag agt tcc cct ccc aga gaa gaa gcg cct | | | 1887 |
| Gln Ser Gln Pro Ala Lys Glu Ser Ser Pro Pro Arg Glu Glu Ala Pro | | | |
| | 590 | 595 | 600 |
| ccc cca cct cct ccg act gaa gac agt tgt gcc aaa aag ccc cgg tct | | | 1935 |
| Pro Pro Pro Pro Pro Thr Glu Asp Ser Cys Ala Lys Lys Pro Arg Ser | | | |
| | 605 | 610 | 615 |
| cgc aca aag atc tcc tta gaa gcc ctg ggg atc ctc caa agc ttt att | | | 1983 |
| Arg Thr Lys Ile Ser Leu Glu Ala Leu Gly Ile Leu Gln Ser Phe Ile | | | |
| | 620 | 625 | 630 |
| cat gat gta ggc ctg tac cca gac cag gaa gcc atc cac act ctt tcg | | | 2031 |
| His Asp Val Gly Leu Tyr Pro Asp Gln Glu Ala Ile His Thr Leu Ser | | | |
| | 635 | 640 | 645 |
| gct cag ctg gat ctc ccc aaa cac acc atc atc aag ttc ttc cag aac | | | 2079 |
| Ala Gln Leu Asp Leu Pro Lys His Thr Ile Ile Lys Phe Phe Gln Asn | | | |
| | 655 | 660 | 665 |
| cag cgg tac cac gtg aag cac cac ggg aag ctg aaa gag cac ctg ggc | | | 2127 |
| Gln Arg Tyr His Val Lys His His Gly Lys Leu Lys Glu His Leu Gly | | | |
| | 670 | 675 | 680 |
| tcc gcg gtg gac gtg gct gaa tat aag gac gag gag ctg ctg acc gag | | | 2175 |
| Ser Ala Val Asp Val Ala Glu Tyr Lys Asp Glu Glu Leu Leu Thr Glu | | | |
| | 685 | 690 | 695 |
| tca gag gag aac gac agc gag gaa ggc tcc gag gag atg tac aaa gtg | | | 2223 |
| Ser Glu Glu Asn Asp Ser Glu Glu Gly Ser Glu Glu Met Tyr Lys Val | | | |
| | 700 | 705 | 710 |
| gag gct gag gag gaa aat gct gac aaa agc aag gca gca cct gcc gaa | | | 2271 |
| Glu Ala Glu Glu Glu Asn Ala Asp Lys Ser Lys Ala Ala Pro Ala Glu | | | |
| | 715 | 720 | 725 |
| att gac cag aga taatgtgaac ttctactagg caaagcaata catcggtcca | | | 2323 |
| Ile Asp Gln Arg | | | |
| 730 | | | |
| aggattttct gctttcattt ctttaaaagt tttttgtag tttgtttttt gtttttgttt | | | 2383 |
| ttgggttttt ttggctttat ttttgccttt ttatgtctgt tttgtttttt ttacoccttt | | | 2443 |
| ggacattttt ttgttgacaca ggatacacct atagactgaa taagttcagt atttccgaat | | | 2503 |
| cagacatcgc cttggcacaag acactaaagc gttacacttt atcccgtctc tatgactgga | | | 2563 |

tcatagtcat tataatcaca ggagactctg ccttcattat ccttgcaactt aacggaagtt 2623
acatcaggca agttccagga tgaaaagaac tatgaaataa atgaaggaag ctacaagtggt 2683
gtgtgtatat gtatatgtat atatctctat atttacatat atatattaaa attgcatggg 2743
acagagactt tgcaatccga aagaatagac tgtgaaatga gttcttaaag aaaagacttg 2803
tttatgtatt aaaaaaacca cttcacagtg agtcgctttg gctttttgat aaactgcggc 2863
ctgctctcag ggtgggggtga ctatttttga atctctatctt attttttctg tttgtccctg 2923
atttttttttt ttaattctat ggcttccctat ctggcagctt aatgggtaat ttttgaggta 2983
tgtatttaac aaaataaacg acaactgccga aaaaaaaaa agtgaagtga aaacaatcag 3043
ggcacattaa aatgatataa gtcaaataaa tottaaagac acaatgcaca cttaaaatga 3103
ctcaataaaa tgacttgcta cgttccgtta ttcaatttgt cattactgta gtgaacagat 3163
gcattttctgt ggaattccaa ataagtaaaa ctgaaattca gtgcagagaa aactttgtcc 3223
actagtgcga gtcttgatca aatgacattt tgacattgga catatggaat tcatagtatg 3283
agccacattt tgttgtgaaa tttatttacc tgcttgtggc ttcaaactctg aaaattaata 3343
agcctgctcg tttaaaagtt gtttgttgtt gctgtttttt tgtctttttg ttttttacta 3403
gaaaatagtt cagtgtataa ttaagttaga aaagaagttg ctgccagtt aaaggggctc 3463
cctctcaaat aaatctccat ccttccctct cccaaaagac atttctgatt tctgcttcac 3523
tttgggcttc ctcttctctg tacacattcc atctacctaa tcaaacattt tcagtccctg 3583
atctctcctg tcccttttcc tgggatgaca gccctaacaa gaactgtttt tgaatcggtg 3643
tgcagctcca ggcaatagag tatgtgaagc gatttcagta gaatcactta ctcatcctaa 3703
aagaaaacat tatcccagtt acctacatcg caattacctt atgtaaagca gaactaatgc 3763
tgactggatg tttaatggga tgagcattaa agctgcaatc tactatagta ctccagatct 3823
ctttcggtt cctatgagaa acaccagaag cattacttcc cacttctact tacagtaatt 3883
gcaagaggag acctcacatt caggactggc ctagtgaacg taatccatgc tttaaactgg 3943
ccattaaaca gtcccacatg gttggatttt tttttttttt ttgagttgtg ctttcacaaa 4003
accttgtaa agacctcatg caatatcact ttgaaagtta ttttctgttt actacacaaa 4063
cattgtaata taactgttaa tactatttat atatttgaaa ggtataaaaag gtaggagtta 4123
aaaaaaaaac ctctatgtgt agatattaac tcagaactta caatatacag ggagaagaca 4183
tgttgcaata caagctaatt ctagctgctc agtaacctct ggagttttta aagggaacatt 4243

ttctgtact ttttcaaata atgatgttta aaaattatct tgacataagc gtcataatacc 4303
 tttgcaaaag gatggttgtt tgcagtttagc cctggcccca tcttctctat ttctgtagta 4363
 tgctgcagct ttaatcagaa agtccatggt tgctgcttcc tgatctccga gttactcttt 4423
 ccaaattgtc ttcttacact gttgctgaag gtcactctgt acacgtaatg gaaactgatt 4483
 ttgccaagct cttacaagggt ggttcatcta tcgatggcat ccgcatttgg tatcttttac 4543
 acttcaacca aaaatttatt aggtattttt caatgctaag tcttgccctt tattttttta 4603
 tttcactgcc aagtttgcag tggttctaag tgaatctgtg ggcatttttag cctgtggtct 4663
 tgccagatct ttgcgaatta caatgcatat atgtctatct attcaatctc tgtcatataa 4723
 tatctatttg gaagaagaaa ctttctcttg tagtgccctc tgacaaagca caatttcccg 4783
 cctttttttt tttttttgtg aaatgaaaaa aacaaattgt gttttattgc ggtatcaaca 4843
 atgtgaataa ggattaacat attgtaaatg ttcttttttc catgtaaatc aactatcttt 4903
 gttatcacta agtgataatt aatttttaac ttatgtgcat tgtaggctg ttagaatttt 4963
 ttggttgta aaataaacgc attcaataaa tatg 4997

<210> 2

<211> 733

<212> PRT

<213> Homo sapiens

<400> 2

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Arg | Arg | Ser | Glu | Ser | Pro | Cys | Leu | Arg | Asp | Ser | Pro | Asp | Arg |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Arg | Ser | Gly | Ser | Pro | Asp | Val | Lys | Gly | Pro | Pro | Pro | Val | Lys | Val | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Arg | Leu | Glu | Gln | Asn | Gly | Ser | Pro | Met | Gly | Ala | Arg | Gly | Arg | Pro | Asn |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gly | Ala | Val | Ala | Lys | Ala | Val | Gly | Gly | Leu | Met | Ile | Pro | Val | Phe | Cys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Val | Val | Glu | Gln | Leu | Asp | Gly | Ser | Leu | Glu | Tyr | Asp | Asn | Arg | Glu | Glu |
| | 65 | | | | 70 | | | | | 75 | | | | 80 | |
| His | Ala | Glu | Phe | Val | Leu | Val | Arg | Lys | Asp | Val | Leu | Phe | Ser | Gln | Leu |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Val | Glu | Thr | Ala | Leu | Leu | Ala | Leu | Gly | Tyr | Ser | His | Ser | Ser | Ala | Ala |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Gln | Ala | Gln | Gly | Ile | Ile | Lys | Leu | Gly | Arg | Trp | Asn | Pro | Leu | Pro | Leu |
| | | 115 | | | | | 120 | | | | | 125 | | | |

Ser Tyr Val Thr Asp Ala Pro Asp Ala Thr Val Ala Asp Met Leu Gln
130 135 140

Asp Val Tyr His Val Val Thr Leu Lys Ile Gln Leu Gln Ser Cys Ser
145 150 155 160

Lys Leu Glu Asp Leu Pro Ala Glu Gln Trp Asn His Ala Thr Val Arg
165 170 175

Asn Ala Leu Lys Glu Leu Leu Lys Glu Met Asn Gln Ser Thr Leu Ala
180 185 190

Lys Glu Cys Pro Leu Ser Gln Ser Met Ile Ser Ser Ile Val Asn Ser
195 200 205

Thr Tyr Tyr Ala Asn Val Ser Ala Thr Lys Cys Gln Glu Phe Gly Arg
210 215 220

Trp Tyr Lys Lys Tyr Lys Lys Ile Lys Val Glu Arg Val Glu Arg Glu
225 230 235 240

Asn Leu Ser Asp Tyr Cys Val Leu Gly Gln Arg Pro Met His Leu Pro
245 250 255

Asn Met Asn Gln Leu Ala Ser Leu Gly Lys Thr Asn Glu Gln Ser Pro
260 265 270

His Ser Gln Ile His His Ser Thr Pro Ile Arg Asn Gln Val Pro Ala
275 280 285

Leu Gln Pro Ile Met Ser Pro Gly Leu Leu Ser Pro Gln Leu Ser Pro
290 295 300

Gln Leu Val Arg Gln Gln Ile Ala Met Ala His Leu Ile Asn Gln Gln
305 310 315 320

Ile Ala Val Ser Arg Leu Leu Ala His Gln His Pro Gln Ala Ile Asn
325 330 335

Gln Gln Phe Leu Asn His Pro Pro Ile Pro Arg Ala Val Lys Pro Glu
340 345 350

Pro Thr Asn Ser Ser Val Glu Val Ser Pro Asp Ile Tyr Gln Gln Val
355 360 365

Arg Asp Glu Leu Lys Arg Ala Ser Val Ser Gln Ala Val Phe Ala Arg
370 375 380

Val Ala Phe Asn Arg Thr Gln Gly Leu Leu Ser Glu Ile Leu Arg Lys
385 390 395 400

Glu Glu Asp Pro Arg Thr Ala Ser Gln Ser Leu Leu Val Asn Leu Arg
405 410 415

Ala Met Gln Asn Phe Leu Asn Leu Pro Glu Val Glu Arg Asp Arg Ile
420 425 430

Tyr Gln Asp Glu Arg Glu Arg Ser Met Asn Pro Asn Val Ser Met Val
 435 440 445
 Ser Ser Ala Ser Ser Ser Pro Ser Ser Ser Arg Thr Pro Gln Ala Lys
 450 455 460
 Thr Ser Thr Pro Thr Thr Asp Leu Pro Ile Lys Val Asp Gly Ala Asn
 465 470 475 480
 Ile Asn Ile Thr Ala Ala Ile Tyr Asp Glu Ile Gln Gln Glu Met Lys
 485 490 495
 Arg Ala Lys Val Ser Gln Ala Leu Phe Ala Lys Val Ala Ala Asn Lys
 500 505 510
 Ser Gln Gly Trp Leu Cys Glu Leu Leu Arg Trp Lys Glu Asn Pro Ser
 515 520 525
 Pro Glu Asn Arg Thr Leu Trp Glu Asn Leu Cys Thr Ile Arg Arg Phe
 530 535 540
 Leu Asn Leu Pro Gln His Glu Arg Asp Val Ile Tyr Glu Glu Glu Ser
 545 550 555 560
 Arg His His His Ser Glu Arg Met Gln His Val Val Gln Leu Pro Pro
 565 570 575
 Glu Pro Val Gln Val Leu His Arg Gln Gln Ser Gln Pro Ala Lys Glu
 580 585 590
 Ser Ser Pro Pro Arg Glu Glu Ala Pro Pro Pro Pro Pro Pro Thr Glu
 595 600 605
 Asp Ser Cys Ala Lys Lys Pro Arg Ser Arg Thr Lys Ile Ser Leu Glu
 610 615 620
 Ala Leu Gly Ile Leu Gln Ser Phe Ile His Asp Val Gly Leu Tyr Pro
 625 630 635 640
 Asp Gln Glu Ala Ile His Thr Leu Ser Ala Gln Leu Asp Leu Pro Lys
 645 650 655
 His Thr Ile Ile Lys Phe Phe Gln Asn Gln Arg Tyr His Val Lys His
 660 665 670
 His Gly Lys Leu Lys Glu His Leu Gly Ser Ala Val Asp Val Ala Glu
 675 680 685
 Tyr Lys Asp Glu Glu Leu Leu Thr Glu Ser Glu Glu Asn Asp Ser Glu
 690 695 700
 Glu Gly Ser Glu Glu Met Tyr Lys Val Glu Ala Glu Glu Glu Asn Ala
 705 710 715 720
 Asp Lys Ser Lys Ala Ala Pro Ala Glu Ile Asp Gln Arg
 725 730

<210> 3
 <211> 2202
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(2199)

<220>
 <221> misc_feature
 <222> (63)
 <223> y represents t/u or c

<220>
 <221> misc_feature
 <222> (60..63)
 <223> Xaa represents any amino acid

<400> 3
 atg gag cgg cgg agc gag agc ccg tgt ctt cgg gac agc ccc gac cga 48
 Met Glu Arg Arg Ser Glu Ser Pro Cys Leu Arg Asp Ser Pro Asp Arg
 1 5 10 15

aga agc ggc agc ccy gac gtc aag ggg cct ccc ccg gtg aag gtg gcc 96
 Arg Ser Gly Ser Xaa Asp Val Lys Gly Pro Pro Pro Val Lys Val Ala
 20 25 30

cgg ctg gag cag aac ggc agc ccc atg gga gcc cgc ggg agg ccc aac 144
 Arg Leu Glu Gln Asn Gly Ser Pro Met Gly Ala Arg Gly Arg Pro Asn
 35 40 45

ggc gcc gtg gcc aag gcc gtg gga ggt ttg atg att cca gtt ttc tgt 192
 Gly Ala Val Ala Lys Ala Val Gly Gly Leu Met Ile Pro Val Phe Cys
 50 55 60

gtg gtg gag cag ttg gat ggc tct ctt gaa tac gac aac cga gaa gag 240
 Val Val Glu Gln Leu Asp Gly Ser Leu Glu Tyr Asp Asn Arg Glu Glu
 65 70 75 80

cac gct gag ttc gtc ttg gtg cgg aaa gat gtg ctt ttt agc cag ctg 288
 His Ala Glu Phe Val Leu Val Arg Lys Asp Val Leu Phe Ser Gln Leu
 85 90 95

gtg gag acc gcg ctc ctg gcc ctg ggg tat tcc cac agc tct gca gcg 336
 Val Glu Thr Ala Leu Leu Ala Leu Gly Tyr Ser His Ser Ser Ala Ala
 100 105 110

cag gcc caa gga ata atc aag cta ggg agg tgg aac ccc ctc ccc ctc 384
 Gln Ala Gln Gly Ile Ile Lys Leu Gly Arg Trp Asn Pro Leu Pro Leu
 115 120 125

agt tat gtg aca gac gcc cct gat gcg act gtg gcc gac atg ctg caa 432
 Ser Tyr Val Thr Asp Ala Pro Asp Ala Thr Val Ala Asp Met Leu Gln
 130 135 140

| | |
|-----------------------------------------------------------------|------|
| gat gtc tat cac gtt gtg acg ctg aag atc caa tta caa agt tgt tca | 480 |
| Asp Val Tyr His Val Val Thr Leu Lys Ile Gln Leu Gln Ser Cys Ser | |
| 145 150 155 160 | |
| aag ttg gaa gac ttg cct gcg gag caa tgg aac cac gcc acc gtc cgc | 528 |
| Lys Leu Glu Asp Leu Pro Ala Glu Gln Trp Asn His Ala Thr Val Arg | |
| 165 170 175 | |
| aat gcc tta aag gaa ctg ctc aaa gaa atg aac cag agc aca tta gcc | 576 |
| Asn Ala Leu Lys Glu Leu Leu Lys Glu Met Asn Gln Ser Thr Leu Ala | |
| 180 185 190 | |
| aaa gaa tgc cct ctc tcc cag agt atg att tca tcc att gta aat agc | 624 |
| Lys Glu Cys Pro Leu Ser Gln Ser Met Ile Ser Ser Ile Val Asn Ser | |
| 195 200 205 | |
| aca tac tat gcc aat gtg tca gca acc aag tgc cag gag ttt ggg aga | 672 |
| Thr Tyr Tyr Ala Asn Val Ser Ala Thr Lys Cys Gln Glu Phe Gly Arg | |
| 210 215 220 | |
| tgg tac aaa aag tat aag aag ata aaa gtg gaa aga gtg gag cga gag | 720 |
| Trp Tyr Lys Lys Tyr Lys Lys Ile Lys Val Glu Arg Val Glu Arg Glu | |
| 225 230 235 240 | |
| aac ctt tca gac tat tgt gtt ctg ggc cag cgg cca atg cat tta cca | 768 |
| Asn Leu Ser Asp Tyr Cys Val Leu Gly Gln Arg Pro Met His Leu Pro | |
| 245 250 255 | |
| aat atg aac cag ctg gca tcc ctg ggc aaa acc aac gaa cag tct cct | 816 |
| Asn Met Asn Gln Leu Ala Ser Leu Gly Lys Thr Asn Glu Gln Ser Pro | |
| 260 265 270 | |
| cat agc caa atc cac cac agt act cca atc cga aac caa gtg ccc gca | 864 |
| His Ser Gln Ile His His Ser Thr Pro Ile Arg Asn Gln Val Pro Ala | |
| 275 280 285 | |
| ctc cag ccc atc atg agc cct ggt ctt ctc tca ccg cag ctc agt cct | 912 |
| Leu Gln Pro Ile Met Ser Pro Gly Leu Leu Ser Pro Gln Leu Ser Pro | |
| 290 295 300 | |
| cag ctt gtc agg cag caa ata gcc atg gcc cat ctg ata aac caa cag | 960 |
| Gln Leu Val Arg Gln Gln Ile Ala Met Ala His Leu Ile Asn Gln Gln | |
| 305 310 315 320 | |
| ata gcc gtt agc cga otc ctg gct cac cag cat cct caa gcc atc aac | 1008 |
| Ile Ala Val Ser Arg Leu Leu Ala His Gln His Pro Gln Ala Ile Asn | |
| 325 330 335 | |
| cag cag ttc ttg aac cac cca ccc att ccc aga gca gtt aag cca gag | 1056 |
| Gln Gln Phe Leu Asn His Pro Pro Ile Pro Arg Ala Val Lys Pro Glu | |
| 340 345 350 | |
| cca aca aac tcc tct gtg gaa gtc tct cct gat atc tac cag caa gtt | 1104 |
| Pro Thr Asn Ser Ser Val Glu Val Ser Pro Asp Ile Tyr Gln Gln Val | |
| 355 360 365 | |

aga gat gag ttg aag agg gct agt gtg tct caa gct gtc ttt gca aga 1152
 Arg Asp Glu Leu Lys Arg Ala Ser Val Ser Gln Ala Val Phe Ala Arg
 370 375 380

gtg gca ttc aac cgc aca cag gga tta ttg tca gag ata ctg cgt aag 1200
 Val Ala Phe Asn Arg Thr Gln Gly Leu Leu Ser Glu Ile Leu Arg Lys
 385 390 395 400

gaa gaa gat ccc agg act gcg tct cag tct ctt cta gta aac ctg agg 1248
 Glu Glu Asp Pro Arg Thr Ala Ser Gln Ser Leu Leu Val Asn Leu Arg
 405 410 415

gcc atg cag aac ttc ctc aac ctg cct gaa gtg gag cgt gat cgc att 1296
 Ala Met Gln Asn Phe Leu Asn Leu Pro Glu Val Glu Arg Asp Arg Ile
 420 425 430

tac cag gat gag cga gag agg agc atg aac ccc aat gtg agc atg gtc 1344
 Tyr Gln Asp Glu Arg Glu Arg Ser Met Asn Pro Asn Val Ser Met Val
 435 440 445

tcc tct gcc tct agc agt ccc agc tcc tcc cga acc cca cag gcc aaa 1392
 Ser Ser Ala Ser Ser Ser Pro Ser Ser Ser Arg Thr Pro Gln Ala Lys
 450 455 460

acc tcg aca ccg aca aca gac ctc cct att aag gtg gac ggc gcc aac 1440
 Thr Ser Thr Pro Thr Thr Asp Leu Pro Ile Lys Val Asp Gly Ala Asn
 465 470 475 480

gtc aac atc aca gct gcc att tat gac gag atc caa cag gag atg aaa 1488
 Val Asn Ile Thr Ala Ala Ile Tyr Asp Glu Ile Gln Gln Glu Met Lys
 485 490 495

aga gcc aag gtg tct caa gcc ctg ttt gcc aaa gtg gct gca aac aaa 1536
 Arg Ala Lys Val Ser Gln Ala Leu Phe Ala Lys Val Ala Ala Asn Lys
 500 505 510

agt cag ggc tgg ctt tgc gaa ctg ctt cgt tgg aag gag aac ccc agc 1584
 Ser Gln Gly Trp Leu Cys Glu Leu Leu Arg Trp Lys Glu Asn Pro Ser
 515 520 525

cca gaa aac cgc acc ctt tgg gag aat ctc tgc acc atc cgc cgt ttc 1632
 Pro Glu Asn Arg Thr Leu Trp Glu Asn Leu Cys Thr Ile Arg Arg Phe
 530 535 540

ctg aat ctt ccc caa cat gag cgg gat gtg atc tat gag gaa gaa tct 1680
 Leu Asn Leu Pro Gln His Glu Arg Asp Val Ile Tyr Glu Glu Glu Ser
 545 550 555 560

cga cat cac cac agt gaa cgc atg cag cat gtg gtc cag ctc cca cct 1728
 Arg His His His Ser Glu Arg Met Gln His Val Val Gln Leu Pro Pro
 565 570 575

gag ccc gtg cag gtc ctt cat cga cag cag tcc cag cca act aag gag 1776
 Glu Pro Val Gln Val Leu His Arg Gln Gln Ser Gln Pro Thr Lys Glu
 580 585 590

agc tcc cct ccc aga gaa gaa gca ccc cca ccg cct cct cca aca gaa 1824

Ser Ser Pro Pro Arg Glu Glu Ala Pro Pro Pro Pro Pro Pro Thr Glu
595 600 605

gac agc tgt gcc aaa aag cct cgg tct cgc aca aag atc tct ttg gaa 1872
Asp Ser Cys Ala Lys Lys Pro Arg Ser Arg Thr Lys Ile Ser Leu Glu
610 615 620

gcc ctg ggc atc ctt caa agc ttc atc cat gat gta ggc ctc tat ccc 1920
Ala Leu Gly Ile Leu Gln Ser Phe Ile His Asp Val Gly Leu Tyr Pro
625 630 635 640

gac cag gaa gcc atc cac aca ctc tcc gcc cag ctg gat ctc ccc aaa 1968
Asp Gln Glu Ala Ile His Thr Leu Ser Ala Gln Leu Asp Leu Pro Lys
645 650 655

cac acc atc atc aag ttc ttc cag aac cag agg tac cac gtg aag cac 2016
His Thr Ile Ile Lys Phe Phe Gln Asn Gln Arg Tyr His Val Lys His
660 665 670

cac ggg aag ctg aaa gag cac ctg ggc tcc gcg gtg gac gtg gct gaa 2064
His Gly Lys Leu Lys Glu His Leu Gly Ser Ala Val Asp Val Ala Glu
675 680 685

tat aag gac gag gag ctg ctg acc gag tca gag gag aac gac agc gag 2112
Tyr Lys Asp Glu Glu Leu Leu Thr Glu Ser Glu Glu Asn Asp Ser Glu
690 695 700

gaa ggc tcc gag gag atg tac aaa gtg gag gct gag gag gaa aat gct 2160
Glu Gly Ser Glu Glu Met Tyr Lys Val Glu Ala Glu Glu Glu Asn Ala
705 710 715 720

gac aaa agc aag gca gca cct gcc gaa att gac cag aga taa 2202
Asp Lys Ser Lys Ala Ala Pro Ala Glu Ile Asp Gln Arg
725 730

<210> 4

<211> 733

<212> PRT

<213> Mus musculus

<220>

<221> misc_feature

<222> (21)

<223> Xaa represents any amino acid

<400> 4

Met Glu Arg Arg Ser Glu Ser Pro Cys Leu Arg Asp Ser Pro Asp Arg
1 5 10 15

Arg Ser Gly Ser Xaa Asp Val Lys Gly Pro Pro Pro Val Lys Val Ala
20 25 30

Arg Leu Glu Gln Asn Gly Ser Pro Met Gly Ala Arg Gly Arg Pro Asn
35 40 45

Gly Ala Val Ala Lys Ala Val Gly Gly Leu Met Ile Pro Val Phe Cys
12

50 55 60
 Val Val Glu Gln Leu Asp Gly Ser Leu Glu Tyr Asp Asn Arg Glu Glu
 65 70 75 80
 His Ala Glu Phe Val Leu Val Arg Lys Asp Val Leu Phe Ser Gln Leu
 85 90 95
 Val Glu Thr Ala Leu Leu Ala Leu Gly Tyr Ser His Ser Ser Ala Ala
 100 105 110
 Gln Ala Gln Gly Ile Ile Lys Leu Gly Arg Trp Asn Pro Leu Pro Leu
 115 120 125
 Ser Tyr Val Thr Asp Ala Pro Asp Ala Thr Val Ala Asp Met Leu Gln
 130 135 140
 Asp Val Tyr His Val Val Thr Leu Lys Ile Gln Leu Gln Ser Cys Ser
 145 150 155 160
 Lys Leu Glu Asp Leu Pro Ala Glu Gln Trp Asn His Ala Thr Val Arg
 165 170 175
 Asn Ala Leu Lys Glu Leu Leu Lys Glu Met Asn Gln Ser Thr Leu Ala
 180 185 190
 Lys Glu Cys Pro Leu Ser Gln Ser Met Ile Ser Ser Ile Val Asn Ser
 195 200 205
 Thr Tyr Tyr Ala Asn Val Ser Ala Thr Lys Cys Gln Glu Phe Gly Arg
 210 215 220
 Trp Tyr Lys Lys Tyr Lys Lys Ile Lys Val Glu Arg Val Glu Arg Glu
 225 230 235 240
 Asn Leu Ser Asp Tyr Cys Val Leu Gly Gln Arg Pro Met His Leu Pro
 245 250 255
 Asn Met Asn Gln Leu Ala Ser Leu Gly Lys Thr Asn Glu Gln Ser Pro
 260 265 270
 His Ser Gln Ile His His Ser Thr Pro Ile Arg Asn Gln Val Pro Ala
 275 280 285
 Leu Gln Pro Ile Met Ser Pro Gly Leu Leu Ser Pro Gln Leu Ser Pro
 290 295 300
 Gln Leu Val Arg Gln Gln Ile Ala Met Ala His Leu Ile Asn Gln Gln
 305 310 315 320
 Ile Ala Val Ser Arg Leu Leu Ala His Gln His Pro Gln Ala Ile Asn
 325 330 335
 Gln Gln Phe Leu Asn His Pro Pro Ile Pro Arg Ala Val Lys Pro Glu
 340 345 350
 Pro Thr Asn Ser Ser Val Glu Val Ser Pro Asp Ile Tyr Gln Gln Val

355 360 365
 Arg Asp Glu Leu Lys Arg Ala Ser Val Ser Gln Ala Val Phe Ala Arg
 370 375 380
 Val Ala Phe Asn Arg Thr Gln Gly Leu Leu Ser Glu Ile Leu Arg Lys
 385 390 395 400
 Glu Glu Asp Pro Arg Thr Ala Ser Gln Ser Leu Leu Val Asn Leu Arg
 405 410 415
 Ala Met Gln Asn Phe Leu Asn Leu Pro Glu Val Glu Arg Asp Arg Ile
 420 425 430
 Tyr Gln Asp Glu Arg Glu Arg Ser Met Asn Pro Asn Val Ser Met Val
 435 440 445
 Ser Ser Ala Ser Ser Ser Pro Ser Ser Ser Arg Thr Pro Gln Ala Lys
 450 455 460
 Thr Ser Thr Pro Thr Thr Asp Leu Pro Ile Lys Val Asp Gly Ala Asn
 465 470 475 480
 Val Asn Ile Thr Ala Ala Ile Tyr Asp Glu Ile Gln Gln Glu Met Lys
 485 490 495
 Arg Ala Lys Val Ser Gln Ala Leu Phe Ala Lys Val Ala Ala Asn Lys
 500 505 510
 Ser Gln Gly Trp Leu Cys Glu Leu Leu Arg Trp Lys Glu Asn Pro Ser
 515 520 525
 Pro Glu Asn Arg Thr Leu Trp Glu Asn Leu Cys Thr Ile Arg Arg Phe
 530 535 540
 Leu Asn Leu Pro Gln His Glu Arg Asp Val Ile Tyr Glu Glu Glu Ser
 545 550 555 560
 Arg His His His Ser Glu Arg Met Gln His Val Val Gln Leu Pro Pro
 565 570 575
 Glu Pro Val Gln Val Leu His Arg Gln Gln Ser Gln Pro Thr Lys Glu
 580 585 590
 Ser Ser Pro Pro Arg Glu Glu Ala Pro Pro Pro Pro Pro Pro Thr Glu
 595 600 605
 Asp Ser Cys Ala Lys Lys Pro Arg Ser Arg Thr Lys Ile Ser Leu Glu
 610 615 620
 Ala Leu Gly Ile Leu Gln Ser Phe Ile His Asp Val Gly Leu Tyr Pro
 625 630 635 640
 Asp Gln Glu Ala Ile His Thr Leu Ser Ala Gln Leu Asp Leu Pro Lys
 645 650 655
 His Thr Ile Ile Lys Phe Phe Gln Asn Gln Arg Tyr His Val Lys His

660 665 670
 His Gly Lys Leu Lys Glu His Leu Gly Ser Ala Val Asp Val Ala Glu
 675 680 685
 Tyr Lys Asp Glu Glu Leu Leu Thr Glu Ser Glu Glu Asn Asp Ser Glu
 690 695 700
 Glu Gly Ser Glu Glu Met Tyr Lys Val Glu Ala Glu Glu Glu Asn Ala
 705 710 715 720
 Asp Lys Ser Lys Ala Ala Pro Ala Glu Ile Asp Gln Arg
 725 730

<210> 5
 <211> 18
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Oligonucleotide Primer

<400> 5
 caatttttgag cccggaag

18

<210> 6
 <211> 22
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Oligonucleotide Primer

<400> 6
 tgactagaaa ggcattccag ag

22

<210> 7
 <211> 25
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Oligonucleotide Primer

<400> 7
 caagaacagc catattgact tgaac

25

<210> 8
 <211> 20
 <212> DNA
 <213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 8
gggtacagcc catgtgtgag

20

<210> 9
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 9
aggtgaccag cagcctct

18

<210> 10
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 10
gtaaaacgga catatcccc

20

<210> 11
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 11
agctataatt gcatcattgc a

21

<210> 12
<211> 19
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 12
tggtctataa cggctctatg

19

<210> 13
<211> 20

<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 13
ctctacagtt tataaccagc

20

<210> 14
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 14
tacactggat tcatattccc

20

<210> 15
<211> 23
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 15
atttcaattt ccaagagctg agg

23

<210> 16
<211> 22
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 16
gctgatgtga cagaaacatc cc

22

<210> 17
<211> 24
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 17
catgacctga aataaacata gaca

24

<210> 18
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 18
agcttttctct gtaggctgtc 20

<210> 19
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 19
aatagagggc ccttgcttaa 20

<210> 20
<211> 22
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 20
tttgggataa aaggatatttt gc 22

<210> 21
<211> 23
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 21
gagtttagacc ccgtctaaaa aaa 23

<210> 22
<211> 23
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 22
actctcatct ccttccttgt tcc

23

<210> 23
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 23
tacaaaagga cttgtccagg g

21

<210> 24
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 24
tcaagattgc cgtgaggt

18

<210> 25
<211> 19
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 25
ggaaggtcca gattagaag

19

<210> 26
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 26
aagggaaata aagagaagca t

21

<210> 27
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 27
caatctccac aagttgctca 20

<210> 28
<211> 23
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 28
gggatagata atttaggagt ggg 23

<210> 29
<211> 23
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 29
gctctagtag gctgggtaca taa 23

<210> 30
<211> 23
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 30
ttccaagaat aatgcaatct cag 23

<210> 31
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 31
ttgttcctac agtattgcgg g 21

<210> 32
<211> 19

<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 32
ccaacccaag atgcaaag

19

<210> 33
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 33
ctattgggggt ttcccaggat

20

<210> 34
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 34
tttccaatat tggggcatgt

20

<210> 35
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 35
cagtagaccg cagccagc

18

<210> 36
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<223> Oligonucleotide Primer

<400> 36
ggaaagcaag aaggagcagg

20

<210> 37
 <211> 19
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Oligonucleotide Primer

<400> 37
 ggactccacc tggaactgc

19

<210> 38
 <211> 21
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Oligonucleotide Primer

<400> 38
 gaaaactcgt agtgagagca g

21

<210> 39
 <211> 2199
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(2199)

<400> 39
 atg gag cgg cgg agc gag agc ccg tgt ctg cgg gac agc ccc gac cgg 48
 Met Glu Arg Arg Ser Glu Ser Pro Cys Leu Arg Asp Ser Pro Asp Arg
 1 5 10 15

cgg agc ggc agc ccg gac gtc aag ggg cct ccc cca gtg aag gtg gcc 96
 Arg Ser Gly Ser Pro Asp Val Lys Gly Pro Pro Pro Val Lys Val Ala
 20 25 30

cgg ctg gag cag aac ggc agc ccc atg gga gcc cgc ggg agg ccc aac 144
 Arg Leu Glu Gln Asn Gly Ser Pro Met Gly Ala Arg Gly Arg Pro Asn
 35 40 45

ggc gcc gtg gcc aag gcc gtg gga ggt ttg atg att cct gtc ttt tgt 192
 Gly Ala Val Ala Lys Ala Val Gly Gly Leu Met Ile Pro Val Phe Cys
 50 55 60

gtc gtg gag cag ttg gac ggc tct ctt gaa tat gac aac aga gaa gaa 240
 Val Val Glu Gln Leu Asp Gly Ser Leu Glu Tyr Asp Asn Arg Glu Glu
 65 70 75 80

cac gcc gag ttt gtc ctg gtg cgg aaa gat gtg ctt ttt agc cag ctg 288
 His Ala Glu Phe Val Leu Val Arg Lys Asp Val Leu Phe Ser Gln Leu

22

| 85 | | | | | | | | | | 90 | | | | | | | | | | 95 | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|--|--|----|--|--|--|--|--|--|--|--|--|--|
| gtg | gag | act | gcg | ctc | ctg | gcc | ctg | ggg | tat | tct | cac | agc | tct | gcg | gcc | | 336 | | | | | | | | | | | | | |
| Val | Glu | Thr | Ala | Leu | Leu | Ala | Leu | Gly | Tyr | Ser | His | Ser | Ser | Ala | Ala | | | | | | | | | | | | | | | |
| 100 | | | | | 105 | | | | | 110 | | | | | | | | | | | | | | | | | | | | |
| cag | gcc | caa | gga | ata | atc | aag | ctg | gga | agg | tgg | aac | cct | ctc | ccc | ctc | | 384 | | | | | | | | | | | | | |
| Gln | Ala | Gln | Gly | Ile | Ile | Lys | Leu | Gly | Arg | Trp | Asn | Pro | Leu | Pro | Leu | | | | | | | | | | | | | | | |
| 115 | | | | | 120 | | | | | 125 | | | | | | | | | | | | | | | | | | | | |
| agt | tat | gtg | aca | gat | gca | ccc | gac | gcg | aca | gtg | gcc | gac | atg | cta | caa | | 432 | | | | | | | | | | | | | |
| Ser | Tyr | Val | Thr | Asp | Ala | Pro | Asp | Ala | Thr | Val | Ala | Asp | Met | Leu | Gln | | | | | | | | | | | | | | | |
| 130 | | | | | 135 | | | | | 140 | | | | | | | | | | | | | | | | | | | | |
| gat | gtc | tat | cat | gtt | gtg | acg | ttg | aaa | atc | caa | tta | caa | agt | tgt | tca | | 480 | | | | | | | | | | | | | |
| Asp | Val | Tyr | His | Val | Val | Thr | Leu | Lys | Ile | Gln | Leu | Gln | Ser | Cys | Ser | | | | | | | | | | | | | | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | | | | | | | | | | | | | | |
| aag | ttg | gaa | gac | ttg | cct | gcg | gag | cag | tgg | aac | cat | gcc | aca | gtc | cgc | | 528 | | | | | | | | | | | | | |
| Lys | Leu | Glu | Asp | Leu | Pro | Ala | Glu | Gln | Trp | Asn | His | Ala | Thr | Val | Arg | | | | | | | | | | | | | | | |
| 165 | | | | | 170 | | | | | 175 | | | | | | | | | | | | | | | | | | | | |
| aat | gcc | tta | aag | gaa | ctg | ctc | aaa | gag | atg | aac | cag | agc | aca | tta | gcc | | 576 | | | | | | | | | | | | | |
| Asn | Ala | Leu | Lys | Glu | Leu | Leu | Lys | Glu | Met | Asn | Gln | Ser | Thr | Leu | Ala | | | | | | | | | | | | | | | |
| 180 | | | | | 185 | | | | | 190 | | | | | | | | | | | | | | | | | | | | |
| aaa | gaa | tgc | cct | ctc | tcc | cag | agt | atg | att | tca | tcc | att | gta | aat | agc | | 624 | | | | | | | | | | | | | |
| Lys | Glu | Cys | Pro | Leu | Ser | Gln | Ser | Met | Ile | Ser | Ser | Ile | Val | Asn | Ser | | | | | | | | | | | | | | | |
| 195 | | | | | 200 | | | | | 205 | | | | | | | | | | | | | | | | | | | | |
| aca | tat | tat | gcc | aat | gtg | tca | gca | acc | aag | tgc | cag | gag | ttt | ggg | aga | | 672 | | | | | | | | | | | | | |
| Thr | Tyr | Tyr | Ala | Asn | Val | Ser | Ala | Thr | Lys | Cys | Gln | Glu | Phe | Gly | Arg | | | | | | | | | | | | | | | |
| 210 | | | | | 215 | | | | | 220 | | | | | | | | | | | | | | | | | | | | |
| tgg | tat | aaa | aag | tac | aag | aag | att | aaa | gtg | gaa | aga | gtg | gaa | cga | gaa | | 720 | | | | | | | | | | | | | |
| Trp | Tyr | Lys | Lys | Tyr | Lys | Lys | Ile | Lys | Val | Glu | Arg | Val | Glu | Arg | Glu | | | | | | | | | | | | | | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | | | | | | | | | | | | | | |
| aac | ctt | tca | gac | tat | tgt | gtt | ctg | ggc | cag | cgt | cca | atg | cat | tta | cca | | 768 | | | | | | | | | | | | | |
| Asn | Leu | Ser | Asp | Tyr | Cys | Val | Leu | Gly | Gln | Arg | Pro | Met | His | Leu | Pro | | | | | | | | | | | | | | | |
| 245 | | | | | 250 | | | | | 255 | | | | | | | | | | | | | | | | | | | | |
| aat | atg | aac | cag | ctg | gca | tcc | ctg | ggg | aaa | acc | aac | gaa | cag | tct | cct | | 816 | | | | | | | | | | | | | |
| Asn | Met | Asn | Gln | Leu | Ala | Ser | Leu | Gly | Lys | Thr | Asn | Glu | Gln | Ser | Pro | | | | | | | | | | | | | | | |
| 260 | | | | | 265 | | | | | 270 | | | | | | | | | | | | | | | | | | | | |
| cac | agc | caa | att | cac | cac | agt | act | cca | atc | cga | aac | caa | gtg | ccc | gca | | 864 | | | | | | | | | | | | | |
| His | Ser | Gln | Ile | His | His | Ser | Thr | Pro | Ile | Arg | Asn | Gln | Val | Pro | Ala | | | | | | | | | | | | | | | |
| 275 | | | | | 280 | | | | | 285 | | | | | | | | | | | | | | | | | | | | |
| tta | cag | ccc | atc | atg | agc | cct | ggg | ctt | ctt | tct | ccc | cag | ctt | agt | cca | | 912 | | | | | | | | | | | | | |
| Leu | Gln | Pro | Ile | Met | Ser | Pro | Gly | Leu | Leu | Ser | Pro | Gln | Leu | Ser | Pro | | | | | | | | | | | | | | | |
| 290 | | | | | 295 | | | | | 300 | | | | | | | | | | | | | | | | | | | | |
| caa | ctt | gta | agg | caa | caa | ata | gcc | atg | gcc | cat | ctg | ata | aac | caa | cag | | 960 | | | | | | | | | | | | | |
| Gln | Leu | Val | Arg | Gln | Gln | Ile | Ala | Met | Ala | His | Leu | Ile | Asn | Gln | Gln | | | | | | | | | | | | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | | | | | | | | | | | | | | |

| | |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| att gcc gtt agc cgg ctc ctg gct cac cag cat cct caa gcc atc aac Ile Ala Val Ser Arg Leu Leu Ala His Gln His Pro Gln Ala Ile Asn 325 330 335 | 1008 |
| cag cag ttc ctg aac cat cca ccc atc ccc aga gca gtt aag cca gag Gln Gln Phe Leu Asn His Pro Pro Ile Pro Arg Ala Val Lys Pro Glu 340 345 350 | 1056 |
| cca acc aac tct tcc gtg gaa gtc tct cca gat atc tac cag caa gtc Pro Thr Asn Ser Ser Val Glu Val Ser Pro Asp Ile Tyr Gln Gln Val 355 360 365 | 1104 |
| aga gat gag ctg aag agg gcc agt gtg tcc caa gct gtc ttt gca aga Arg Asp Glu Leu Lys Arg Ala Ser Val Ser Gln Ala Val Phe Ala Arg 370 375 380 | 1152 |
| gtg gca ttc aac cgc aca cag gga ttg ttg tct gag att ctg cgt aag Val Ala Phe Asn Arg Thr Gln Gly Leu Leu Ser Glu Ile Leu Arg Lys 385 390 395 400 | 1200 |
| gaa gaa gac cct cgg aca gcc tct cag tct ctt cta gta aac ctg agg Glu Glu Asp Pro Arg Thr Ala Ser Gln Ser Leu Leu Val Asn Leu Arg 405 410 415 | 1248 |
| gcc atg cag aat ttc ctc aat ctg cca gaa gtg gag cga gat cgc atc Ala Met Gln Asn Phe Leu Asn Leu Pro Glu Val Glu Arg Asp Arg Ile 420 425 430 | 1296 |
| tac cag gat gag agg gag cgg agc atg aat ccc aat gtg agc atg gtc Tyr Gln Asp Glu Arg Glu Arg Ser Met Asn Pro Asn Val Ser Met Val 435 440 445 | 1344 |
| tcc tcg gcc tcc agc agt ccc agc tcc tcc cga acc cct cag gcc aaa Ser Ser Ala Ser Ser Ser Pro Ser Ser Ser Arg Thr Pro Gln Ala Lys 450 455 460 | 1392 |
| acc tcg aca ccg aca aca gac ctc cct att aag gtg gac ggc gcc aac Thr Ser Thr Pro Thr Thr Asp Leu Pro Ile Lys Val Asp Gly Ala Asn 465 470 475 480 | 1440 |
| atc aac atc aca gct gcc att tat gac gag atc caa cag gag atg aaa Ile Asn Ile Thr Ala Ala Ile Tyr Asp Glu Ile Gln Gln Glu Met Lys 485 490 495 | 1488 |
| agg gcc aag gtg tct caa gcc ctg ttt gcc aaa gtg gct gca aat aaa Arg Ala Lys Val Ser Gln Ala Leu Phe Ala Lys Val Ala Ala Asn Lys 500 505 510 | 1536 |
| agt cag ggc tgg ctg ^o tgt gaa ctg ctc cgc tgg aag gag aac cca agc Ser Gln Gly Trp Leu Cys Glu Leu Leu Arg Trp Lys Glu Asn Pro Ser 515 520 525 | 1584 |
| cca gaa aac cgc acc ctc tgg gaa aac ctc tgt acc atc cgt cgc ttc Pro Glu Asn Arg Thr Leu Trp Glu Asn Leu Cys Thr Ile Arg Arg Phe 530 535 540 | 1632 |

| | |
|-----------------------------------------------------------------|------|
| ctg aac ctt ccc cag cat gag agg gat gtc atc tat gag gag gag tca | 1680 |
| Leu Asn Leu Pro Gln His Glu Arg Asp Val Ile Tyr Glu Glu Glu Ser | |
| 545 550 555 560 | |
| agg cat cac cac agc gaa cgc atg caa cac gtg gtc cag ctt ccc cct | 1728 |
| Arg His His His Ser Glu Arg Met Gln His Val Val Gln Leu Pro Pro | |
| 565 570 575 | |
| gag ccg gtg cag gta ctt cat aga cag cag tct cag cca gcc aag gag | 1776 |
| Glu Pro Val Gln Val Leu His Arg Gln Gln Ser Gln Pro Ala Lys Glu | |
| 580 585 590 | |
| agt tcc cct ccc aga gaa gaa gcg cct ccc cca cct cct ccg act gaa | 1824 |
| Ser Ser Pro Pro Arg Glu Glu Ala Pro Pro Pro Pro Pro Pro Thr Glu | |
| 595 600 605 | |
| gac agt tgt gcc aaa aag ccc cgg tct cgc aca aag atc tcc tta gaa | 1872 |
| Asp Ser Cys Ala Lys Lys Pro Arg Ser Arg Thr Lys Ile Ser Leu Glu | |
| 610 615 620 | |
| gcc ctg ggg atc ctc caa agc ttt att cat gat gta ggc ctg tac cca | 1920 |
| Ala Leu Gly Ile Leu Gln Ser Phe Ile His Asp Val Gly Leu Tyr Pro | |
| 625 630 635 640 | |
| gac cag gaa gcc atc cac act ctt tcg gct cag ctg gat ctc ccc aaa | 1968 |
| Asp Gln Glu Ala Ile His Thr Leu Ser Ala Gln Leu Asp Leu Pro Lys | |
| 645 650 655 | |
| cac acc atc atc aag ttc ttc cag aac cag cgg tac cac gtg aag cac | 2016 |
| His Thr Ile Ile Lys Phe Phe Gln Asn Gln Arg Tyr His Val Lys His | |
| 660 665 670 | |
| cac ggg aag ctg aaa gag cac ctg ggc tcc gcg gtg gac gtg gct gaa | 2064 |
| His Gly Lys Leu Lys Glu His Leu Gly Ser Ala Val Asp Val Ala Glu | |
| 675 680 685 | |
| tat aag gac gag gag ctg ctg acc gag tca gag gag aac gac agc gag | 2112 |
| Tyr Lys Asp Glu Glu Leu Leu Thr Glu Ser Glu Glu Asn Asp Ser Glu | |
| 690 695 700 | |
| gaa ggc tcc gag gag atg tac aaa gtg gag gct gag gag gaa aat gct | 2160 |
| Glu Gly Ser Glu Glu Met Tyr Lys Val Glu Ala Glu Glu Glu Asn Ala | |
| 705 710 715 720 | |
| gac aaa agc aag gca gca cct gcc gaa att gac cag aga | 2199 |
| Asp Lys Ser Lys Ala Ala Pro Ala Glu Ile Asp Gln Arg | |
| 725 730 | |

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.